GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Listing first.45 summaries
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1: gb_bal:*
2: gb_ba2:*
3: gb_ba3:*
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555
1 ATGTCTTTAAACAAGCACTC.....AATCATACACTAAACGATAG 555
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Result	Score	Query Match	Query Match Length DB	DB	ID	Description
C	48.2	8.7	217412	69	AC024400	AC024400 Homo sapi
o.	47.8	8.6	14001	6	PECOMPIRB	x95276 P.falciparu
a	47.6	8.6	192929	60	AC005505	AC005505 Plasmodiu
0 4	47.6	8.6	256172	60	AC005139	AC005139 Plasmodiu
C	47.6	8.6	310779	60	AC005140	AC005140 Plasmodiu
c	47.2	8.5	108908	6	PFMAL3P8	AL034560 Plasmodiu
~1	47.2	8.5	298469	4	AE003846	AE003846 Drosophil
~	45.6	8.2	21595	64	AC014617	AC014617 Drosophil
a	45.6	8.2	193742	82	AL513530	AL513530 Homo sapi
c 10	45.2	8.1	3171	σ	DDU68754	U68754 Dictyosteli
11	45	8.1	179401	62	AC010903	AC010903 Homo sapi



AUTHORS	SULT 1 024400/c CCUS FINITION CESSION RSION RSION RSION COMPANION CESSION COMPANION CO	112 113 114 115 116 117 117 118 118 119 119 119 119 119 119 119 119
Birren, B., Lint Anderson, S., Ba Boukhgalter, B., Choepel, Y., Col DeArallano, K., Fenestor, J., Fe Galagan, J., Gar Grand-Pierre, N. Howland, J.C., I. Klein, J., Lande Lieu, C., Liu, G. MCEwan, P., MCGu Meneus, L., Miho Norman, C.H., O' Peterson, K., Pi Riley, R., Rogovo Severy, P., Spen Subramanian, A.,	ACO24400 Homo sapie ACO24400 ACO24400.2 HTG; HTGS_ human Homo sapie Eukaryota; Mammalla, 1 (bases Birren, B., Homo sapie	
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Birren, B., Linton, L., Nusbaum, C., Lande Anderson, S., Baldwin, J., Barna, N., Bed Boukhgalter, B., Brown, A., Burkett, G., Choepel, Y., Colangelo, M., Collins, S., Choepel, Y., Colangelo, M., Collins, S., Choepel, Y., Colangelo, M., Collins, S., Colenta, J. S., Dod Fenestor, J., Ferreira, P., FitzHugh, W., Grand-Pierre, N., Grant, G., Hagos, B., He Howland, J.C., Iliev, I., Johnson, R., Jon Klein, J., Landers, T., Largocque, K., Leh Klein, J., Landers, T., Largocque, K., Leh Klein, J., Landers, T., McKernan, K., McChwan, P., McGurk, A., McKernan, K., McChwan, C., Liu, G., Locke, K., Macdonald, P., McEwan, P., McGurk, T., Miranda, C., Mleng Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pisani, C., Poll Riley, R., Rogov, P., Rothman, D., Roy, A., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S.,	DNA 139D4 139D4 139D4 139D4 139D4 139D4 139D4 139D4	AC021920 HASMT AC027632 AC003991. PFMAL13P6 CNS071NH FR151J19 AC021920 AC021920 AC021920 AC021920 AF08391 AC021925 PFSTARP AF271619 AF083031 AC004157 CNS018QK AC007926
Nusbaum,C., Lander,E., Abraham,H., Allen,N., J., Barna,N., Beda,F., Boguslavkiy,L., A., Burkett,G., Campopiano,A., Castle,A., M., Collins,S., Collymore,A., Cooke,P., M., Collins,S., Collymore,A., Cooke,P., M., Collins,S., Collymore,A., Cooke,P., M., Collins,S., Collymore,A., Cooke,P., M., Collins,S., Dodge,S., Domino,M., Doyle,M., P., FitzHugh,W., Forrest,C., Gage,D., Ginde,S., Goyette,M., Graham,L., M., Haggos,B., Heaford,A., Horton,L., Johnson,R., Jones,C., Kann,L., Karatas,A., Largocque,K., Lehoczky,J., Levine,R., M., Macdonald,P., Marquis,N., McCarthy,M., M., Macdonald,P., Marquis,N., McCarthy,M., M., Macdonald,P., Marquis,N., Meddrim,J., M., Macdonald,P., Marquis,N., Neddrim,J., M., Macdonald,P., O'Neil,D., Olivar,T.M., J., O'Donnell,P., O'Neil,D., Olivar,T.M., J., Pisani,C., Pollara,V., Raymond,C., Othman,D., Roy,A., Santos,R., Schauer,S., Stange-Thomann,N., Stojanovic,N., as,J., Tesfaye,S., Theodore,J., Tirrell,A.,	LOW-PASS SEQUE raniata; Verte atarrhini; Hon and Lander, F RP11-439D4	AC021920 Homo sapi D31785 Pichia cana AC027632 Homo sapi AC027632 Homo sapi AC003991 Human BAC AL049183 Plasmodiu AL021331 Polone BAO AL021331 Polone BAO AL021331 Polone Sapi AE001566 Plasmodiu AC021920 Homo sapi AE0021925 Plasmodiu Z95276 P.falciparu AF209925 Plasmodiu Z26314 P.falciparu AF209925 Plasmodiu Z26314 P.falciparu AF209925 Plasmodiu Z86314 P.falciparu AF209925 Plasmodiu Z871619 Aspergill AF088391 Trypanoso AL110675 Botrytis AC004157 Plasmodiu U87145 Toxoplasma AC088397 Trypanoso AC007926 Trypanoso AC007926 Trypanoso AC007926 Trypanoso AC007926 Trypanoso AC007926 Trypanoso AC007938 Homo sapi AC011718 Homo sapi AC013194 Homo sapi AC01394 Homo sapi AC01394 Homo sapi AC01394 Homo sapi AC01395297 Try end of AL1398297 Try end of AL192832 T3 end of AL192832 T3 end of AL192832 T3 end of AL192833 Astasia lon AC024860 Caenorhab
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 10, 2000 this sequence version replaced gi:7108401. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
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                                                                                                                                11798 11897: gap of 170 bp 11898 11897: gap of 100 bp 12659: contig of 762 bp 12660 12759: gap of 100 bp 12760 13535: contig of 776 bp 13536 13635: gap of 100 bp 13536 14455: gap of 1720 bp 14456
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10928 10279: gap of

10928 11797: conv-

11797: conv-

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                                15219 15318: gap of 100 bp 15319 16081: contig of 763 bp 16082 16181: gap of 100 bp 16182 16943: contig of 762 bp 16944 17043: gap of 100 bp 17044 17768: contig of 725 bp
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25443: con
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23743: contig of
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43: gap of
24584: contig of 741 bp
100 bp
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46842: contig of 769
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40007: contig of 760 bp in length
107: gap of 100 bp
40835: contig of 728 bp in length
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36534: contig of 760
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34840: contig of 784 bp
40: gap of 100 bp
35674: contig of 734 bp
                                                                                                                                                                                                                                                                                                                                  100 bp 33956; contig of 748 bp in length
                                                                                                                                                                                                                                                                                                                                                                            68: gap of 100 bp in length 31438: contig of 770 bp in length 100 bp
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27124: contig of 754 bp
                         92: gap of 100 r
48553: contig of 761
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45108: contig
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43385: contig of 738 bp
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42547: contig of 770
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41677: contig of 742 b
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33108: contig of 730
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29695: contig of 784
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28811: contig of 731 bp
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21151: contig
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X95276.1 GI:1171591

X95276.1 GI:1171591

gene; LSU rRNA gene; ORF105; ORF129; ORF78; ORF79; ORF91; rp

gene; rpl16 gene; rpl2 gene; rpl23 gene; rpl36 gene; rpL4 gene;
rpl6 gene; rps11 gene; rps12 gene; rps17 gene; rps19 gene; rps3

gene; rps4 gene; RPS5 gene; rps7 gene; rps8 gene; tRNA-Asp;
tRNA-Cys; tRNA-G1n; tRNA-G1n; tRNA-G1y; tRNA-His; tRNA-Leu;
tRNA-Lys; tRNA-wet; tRNA-Phe; tRNA-Pro; tRNA-Ser; tRNA-Thr;
tRNA-Trp; tRNA-Tyr; tufa gene.

malaria parasite P. falciparum.
                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium 1 (bases 1 to 14001) Wilson,R.J.M., Denny,P.W., Preiser,P.R., Rangachari,K., RobRoy,A., Whyte,A., Strath,M., Moore,D.J., Moore,P.W. and
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/product="transfer RNA-Tyr" 14571541	1457. 15441 167. 15441 Genea ^{#†} +RNA-Tvr [#]		/gene="trNA-Met (1)" /product="transfor RNA-Met (1)"	/gene≖"tRNA-Leu" 13731452	/product="transfer RNA-Leu" 13181366		1318. 1306	11841317	,		/product="transfer RNA-Leu" 11481183	/note="extein 1"	11481183	10721142 /gene="trna-cvs"	/gene="tkna-cys" /product="transfer RNA-Cys"	10721142	/gene="tRNA-His"	duct="transfer RNA-His"	981 1053		/db_xref="SPTREMBL:Q25804" /translation="MIKFLKPKIKILKKLNIPFLLYLSGKYNYKCLNYKISYKSYFDL	/processnd="campa_0.1" /db_xref="g1:1171592"	/codon_start=1	340966 /gene="rps4"	/gene="rps4"		/product="transfer RNA-Thr" 242314	/gene="tRNA-Thr"	/gene="ISU rRNA"	/product="large subunit ribosomal RNA"	/qene="LSU rrna"	-+ 4	/db_vref="taxon:5833" /dev stef="taxon:5833"	/organism="Plasmodium falciparum" /strain="C10"		sequences x90351-x90354 (incl.), and	Submitted (23-JAN-1996) R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London NW7 laa, HK	Direct Submission	2 (bases 1 to 14001)	J. Mol. Biol. 261 (2), 155-172 (1996)	Plasmodium falcinarum
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J8394483 /gene="rps3"	/GD_XTEL="SPTKEMAL:Q23808" /translation="MIKLYWLKITINNKYIFININKYKYNKNLILNIYNKNLYIYKKL	/bc/cell_ld="cAA04300/l" /db_xref="GBTDEWT'.OSE000"	/codon_start=1	35573829 /gene="rps19"	35573829 ' /gene="rps19"	PSKQCKYININNFCYIGVNSNIFHNKFKIKNAGYNIYYNIKPKVRGKAKNVCDHPHGG GKGKTGIGRKYPCSKKGLHSKGYKTIK"	TNINNIKTGSY IQLKYCKLGTY IYNISKDYKKGSIFARSAGTFAQILSFYKNLVY TNINNIKTGSY IQLKYCKLKNY FKNTY IGCILY LSKLNNLQXFII IQHNYMINSI	/translation="MILKLKKYNTYKYFKSFGKNNKGYITIYNKGGGNLKYNYKL	/db_xref="GI:1171595" /db_xref="SPTREMBL:025807"	/protein_id="CAA64579.1"	/gene="rp12" /codon_start=1	/genem:rpiz: 27993536	27993536	/translation="MKEVILNFYLYNILFYKINVLNKFCIIYSIKYFTKLDIKYIIKN	/db_xref="GI:1171594" /db_xref="SPTREMBL:Q25806"	/protein_id="CAA64578.1"	/gene="rpl23"	/gene= 1p123	25752802	LYIYNIYMYKHTKNKSKYYFSNKKIRYQKGLGKARLKNFKSPYCKQGACNFGPFYKEN KIISKINYRLIFYYLLINKRSNIIIIKLENIINLLNIFYKNKNYCIFKLLYLKGIINN KYILINLNNKLFNKNIFINIIMYNYLIFLI"	/db_xref="SPTREMBL:Q25805" /translation="MNIIILNNNTLNNIIFKYKYNFFIKLYFNNYIKICKLIIYIIKY	/protein_id="CAA64577.1" /db_xref="GI:1171593"	/codon_start=1	19992571 /genp="rp 4"	19992571 /gene="rpl4"	/gene="tRNA-pro"	/product="transfer RNA-Pro" 1901 1972	19011972 /gene="tRNA-Pro"	/gene-"tRNA-Glu"	/product="transfer RNA-Glu"	1819 1888 /gene="trna-glin"	/genemmtRNA-Lysm	/product="transfer RNA-Lys"	1739 . 1811	/gene∝"tRNA-Asp"	/product="transfer RNA-Asp"	16531728	15551646 /qene="tRNA-Ser"	/gene="tkNA-Ser" /product="transfer RNA-Ser"	1555. 1646	/~>>>=

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/translation="MGQKVHPLIFFGLIYKNYLNNFYINIKKYIFILLNYFNYYYYNY
NMYRICNYKEDNYINININYINYXYIKKYYIKYKSLKILIFDYLYNNILKKNNFNIKGLK
YNYMCFLKIKYVNNINNINYINYXYIKKYYIKYKSLKILIFDYLYNNILKKNNFNIKGLK
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/translation="MNIKIGYVIKNLNINIKIVCISFYKYNFKYKKLLLCNLYIKIYD
NRNEIIINDYILFKYYKKSKYCNNKVIKIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="rpl14"
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/db_xref="GI:1171599"
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/db_xref="GI:1171598"
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/db_xref="GI:1171597"
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Pred. No. 2.3;
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TITLE
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Best Local Similarity
Matches 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   94
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                                         TCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATACTTGACAAA
                                                                                                                      GTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTC
                                                                                                                                                                                                   GGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGTATGTGTAAATGTGAATGTAGTTATGGGTATATATATATATATATGTGTAAATGTC
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TCATGGATAGCTGTTCTACTAATAATAGGTCATATTGCAATGTGGTATCTACACTTTGCT
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On Aug 12, 2000 this sequency version replaced 91:8810446.

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 192929)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Kurdi, O.B., Conway, A.B. and Davis, R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC005505 192929 bp DNA
Plasmodium falciparum chromosome 12 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyman, R.W., Qin, F., Fung, E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria parasite P. falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the finished sequence as soon as it is available the accession number will be preserved.

1 192929: contig of 192929 bp in length.
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1. .192929
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/chromosome="12"
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Pred. No. 2;
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                                     TCGTCATGGTTTAATATAGGAATAATGCATTAAGCGATCTAGGACATGCTGTTAAAAGC 153
AGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTATAGTT
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On Apr 2, 1999 this sequence version replaced gi:4337170.
On Apr 2, 1999 this sequence version replaced gi:4337170.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* is not known and their order in this are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-JUN-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACO05139 256172 bp DNA HTG 01-APR-1999 Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hyman,R.W., Fung,E.L., Qin,F., Tamaki,T., Kurdi,O.B. and Davis,R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malaria parasite P. falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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/db_xref="taxon:5833"
/chromosome="12"
26900 c 25826 g 101937 t And
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                                                                                                                                                                                                                      8.6%;
43.6%;
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248106: contig of 36368 bp in length
248306: gap of unknown length
256172: contig of 7866 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159045: gap of unknown length
211538: contig of 52493 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126535: contig of 126535 bp in length
126735: gap of unknown length
158845: contig of 32110 bp in length
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Pred. No. 2;
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AC005140/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 GTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTC 333
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Submitted (18-JUN-1998) Stanford DNA Sequencing and Technology Submitted (18-JUN-1998) Stanford DNA Sequence (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC005140 310779 bp DNA
Plasmodium falciparum chromosome 12 clone
PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on Aug 12, 2000 this sequence version replaced gi:8810455
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 310779)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
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malaria parasite P. falciparum
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187509
257821
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                                                                       /organism="Plasmodium
/db_xref="taxon:5833"
                                                                                                                                                      1. .310779
/clone-"PFYACB8-420"
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mes 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        PFMAL328 108908 bp DNA INV Plasmodium falciparum MAL3P8, complete sequence. AL034560 AL008968 AL010134 AL010151 AL010159 AL0 AL010209 AL021886 AL021887 297346
                                                                                                               Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,
Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., Mc
Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A.,
Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squar
                                                                                                                                                                                                                                                                                                                    AL034560.3 GI:4725993
HTG; alpha/beta hydrolase; guanine nucleotide-binding protein; long-chain-fatty-acid-CoA ligase; R-FA3; rep11; rep20; rifin;
                   99376085
                                                                                               Rajandream, M.-A., Rutter, S., Skelton, J., Sonston, J.E., Whitehead, S., Woodward, J.R.,
                                                                                                                                                                               Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,
                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium 1 (bases 1 to 108908)
                                                                                                                                                                                                                                                        Plasmodium falciparum
                                                                                                                                                                                                                                                                          pseudogene.
malaria par
                                                                                                                                                                                                                                                                                                          Serine/threonine
                                     Nature
                                                               The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                   Barrell,B.G.
                                                 falciparum
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milarity 43.6%;
Conservative
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Pred. No. 1.9;
D; Mismatches 274;
                                                                                                 Squares, R., ... Newbold, C.
                                                                                                                                                                                                                                                                                                    rep11; rep20; rifin;
telomere: R-CG7; var;
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                                                                                                                                                 S., McLean, J.,
                                                                                                                 Squares, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB10 1SA, 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: The see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 108908)
Lawson,D., Bowman,S., Rajandream,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bowman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           onger because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1SA, UK
                                                                                                                                                                                                                                              ETFFLMKYKVDKEKEDKEKNGRNMVVYTSPVPNDLYEKLKKGEIPDDFLRQMFYTLA
DYKDLILFSGDKDNKNGYNDILSGDKELIBEREKEIKGAIEKHESNSYKTPSTSGNDAKT
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10610. .30944
/note="rep20"
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VKPCIDLINAFERSIHCNEPONSGOKKUYERDVYVCLLDKLEKEAKKCEOKHQNGSONG
OPCEGSTPPDDEEEELLEEDEONTYGKEKVGNKAPAICGDVEEOKEKEEGDCDKAVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIKRAYGKNOTTKETSNGFINNLYVODFYSKLQQTYGSVDKFLKLNDEAICKKHPE
VEEKTDVNFNENLDDIFSHTKYCQACFLGLENDSPRAFKFERECRDQOIRNFDDNE
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DSDTGGNGEKEDSRSEEEEEVSGSGDQGSPPAPPPESPQEKAPAPAPEELPPGPERP
                                                                                                                                                 RKWIERKKIEFEEQENAYEEQQKKNCYNGNNKGGYNGYCGKLEENAAGFLQKLGSCKK
DSGEDNGNGNEEDKLNFRQPNYTFRPAENCKPCSLIEIKCKNGYCNGDPTKGECNGET
YTAEBIEKMNDLNGNIDMLYSDNGKNEIPEDLKSSCKDANIFKGIREDYWKCGKFRDY
                                                                                                                                                                                                                                                                                                                                                                                                                TAASQGSGEAAQPVTVTQPQASGGNTQVAVSPGGAASSTSTTESSQLLRQAFIESAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                             EACKQKYQYGKEKFPNWKCVPTTRGSGEPTGSSGSICVPPRRRRLYVTPLTRLAGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKTGQPRAEDEEDSPRPDAGAGEVDDEDDDADNDDEITPRDLNI EVDDLDSKDPEDQV
EEEKAKDNTDETVETAKETKEDTDRKGEEKQPKEEVDNVKPCEIVKTLFTNGDNTALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLKNGKTNG I EERYGNDPDFFOLREDWWTANRETVWKA I RCSAPRDADY F I KTVCSGG
KTPTQGKCRCIDFSVPTYFDY V PQYLRWFEEWAEDFCKLRKHKLQNAKNKCREKHKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a multi-gene family, donor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDCFQKWGVRKTKEWQQVKAHYEKEDFGKGLTPYKTLEWVLDLSYFPIIKEAHPKEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKLYCDLNGFDCTQTARGKNKYKYEHDCIECYSSCDHFVHWIDNQKKEFEKQKNKYDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDHDKYKETNDSSQLCTMLARSFADIGDIIRGKDLYRGNNGKDKLEENLKTIFGKIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECDDSKIKGSNGGACAPFRRUNLCVRNLENINNYGKINNDTLLADVCLAALHEGDSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB39115.2"
/db_xref="GI:7264037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PFC0005w, MAL3P8.1"
/note="PFC0005w, MAL3P8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQKMEETIKKNQENTSRVTKQNNSTTKFLQQELQEANNCLQKRKQDCKPPQQSAEEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVRTLDPEEELRGIEDTTAKHIFDRIGKIVHEKAKKNAEQYRSQ
LKGSLLKATFEKAPAGQQTPGNTCELKYQWHTNVTKGGNKEYPCRNGTEKRFSEVSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PFC0005w (MAL3P8.1), var gene (3D7-varT3-1), 2009 aa; Similarity to P.falciparum PfEMP-1 gene. Pamulti-gene family, donor sequence corrected"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="R-CG7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:097324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PFC0005w, MAL3P8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(33641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="PFTelo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="MAL3P8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .108908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .38959,39848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lawson, D., Quail, M. and Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        falciparum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .41158)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   len:
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(52066. .53076,53192. .53260))
/gene="PFC0030c, MAL3P8.5"
complement(join(52066. .53076,53192. .53260))
/gene="PFC0030c, MAL3P8.5"
/note="PFC0030c (MAL3P8.5), rifin, (3D7-riff3-2), le
aa; Similarity to other P.falciparum rifins. Member
moddle gene family; predicted using hexexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(48956. .49777,49881. .49949))
/gene="PFC0025c, MAL398.4"
complement(join(48956. .49777,49881. .49949))
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/note="PFC0025c (MAL398.4), stevor (3D7-stevorT3-1),
296 aa; Similarity to other P.falciparum stevors. Mer
of a multi-gene family; predicted using hexExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(43045. .43971,44202. .44255))
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complement(join(43045. .43971,44202. .44255))
/gene="PFC0010c, MAL3P8.2"
/note="PFC0010c (MAL3P8.2), rifin (3D7-riff3-1), len:
aa; Similarity to other P.falciparum rifins. Member of
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join(58103 .58174,58338, .59390)
/gene="PFC0035c"
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TANISAAGVKAGEATGKVLVISGLKKMGISTLGGKNLESYFATTSYKKVASIAQAVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEYEBMDINDIYVPGSPKYKTLIEVVLEPSGNNTTASGKNTPSDTQNDIQNDGIPSDT
PNTPSDIPKTPSDTPPPITDDEWNTLKDEFISQYLQSEQPNDVENDYKSGNSSTNTNI
TTTSHHVVEKKPFIMSIHDRULYTGEBYNYDMSNNSGIYPSSSNRDSLSGTKVPYSGI
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HKWLDTHRDMCEKLKNDNERLAKLKEEWENTHSGNIHTSDSNKTLNTDYSIQIDMDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHMINHKSMSSALTALGTVGCAADYASGATSASAIFLPCGIAALVLLILTVLLIILYI
WLYRRKKRSWKHECKKHLCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="kkmyylkmllftelintlilphyenylnndynysfionntkrtt
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TKGRDKYLKHLKGRCTRGIYECSLGSYILTYIGTTAAKGAAISTAGAGSKNCIYAISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(46448. .47828)
/gene="PFC0015c"
/note="PFC0015c varC pseudogene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (46448. .47828)
/gene="PFC0015c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGWTNYVTQTALQKGIEAGVKAGIEELKGFPGLRKLIKVSQIQSFINPANYAEETTYF
NFIKQVENTKCVVKEHTFCYSTYISKENALSQRASEIAKNAADMAKLAEREVLDKAAP
VTSCLNTAIIASIVAILVIVLVMIIIYLFLRYRKNKKMKKKLQYIKLLEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="Sptrembl:097325"
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/translation="MKIHYINILLFELPLNILIYNQRNHYITRTPKATTRTLCECELY
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                                                                                                                        IYLILRYRRKKKMKKKAQYTKLLNE"
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/db_xref="GI:4494023"
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/db_xref="GI:4494022"
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/db_xref="GI:4494021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multi-gene family; predicted using hexexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVNTKLVKEKYPIADVWDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKPKKEFTNMDTILEDLDKYNEPYYDVQDDIYYDVNDHDVSTVDSNAMDIPSKVQIEN
                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:097326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 38965
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VERSION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TGTTAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGATACTAAT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAAT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCAT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATACATACATATATATATATATATAAGAAGGTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTTCGACGAAGTATATGGTTGGATACA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTTGACAAATCATGGATAGCTGTTCTACTAATAATAGGTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGAATATTATTACTATAGTTTTTATAATTTTTTCTTAAAAACATACTTTTTGGATTATAT 72992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATATAGCATGTGTATATATAGAAATTATGTTTTACTACCAGTACTATGTTTTCTGTTT 73052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTAATATTTTAATTTAAGGAACATATGTTTTAAGAATATTTCTTTGTATTTTATATAGT 73112
                                                                                                                                                                                                                                                                                                                                          AE003846 298469 bp prosophila melanogaster g of 2, complete sequence. AE003846 AE002804 AE003846.2 GI:10728138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136;
1 (bases 1 to 298469)
Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,
                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyco
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                     HTG
                                                                                                                                                                                                                                                                                        fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAPGTTPIETVLNGIVEGTKEAADVAAEAARESATNAIKVQETRLLEAGFNSSISSIN ASIIALVVIILIMVIIYFILBYRRKKKLKKKQYIKLLEE"
join(61248. .61301,61548. .62459)
/gene="PFC0040w,MAL3PB.7"
/gene="PFC0040w,MAL3PB.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDKIEKELNEKFATLQTDIHSDAIPTCICKTSMADKVEKTCLKCTQNLGGIVAPSSGV
LAGIAEGALYAWKPNALQTAIEAALKAAADDILVGGIEAGKKVVIGGLDALEIEKLGI
GSWEPYFTEGYCINVKSLASIIYEKRQTLCGATKSTLDKATCEQIGISIGTMQHDGTY
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aa; Similarity to other P.falciparum rifins. Memb
multi-gene family; predicted using hexExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKIHYINILLFALPLNILVNNQRNHNNSTYHTSNTKTIKSHRSL
CECKLYAQSNYENDQEMKDVIKEFNDRTAQRFEEYNERMQVKKNQCKEQCDKEIQQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CECELYMHNYDNDPEMKRVMQQFHDRTTQRFQEYDERLQEKRQVCKDTCDKEIEKIIL
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/db_xref="GI:4494024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB39120.1"
/db_xref="GI:4494025"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:097328"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%;
47.9%;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                        DNA INV 04-OCT-2000 genomic scaffold 142000013386051 section 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72948
                                                                                                                                                                                                    Brachycera;
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                                                                                                                                                                                                                               Insecta;
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X. Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
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On Oct 9, 2000 this sequence version replaced gi:7304344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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ams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="CG17469 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'map="102E1-102E3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Chromosome="4"
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LFNDNILQKTKTTSTILNKFREMEDOKMSDQKKKNPKPLKKGFTPPPEISHQFIRSDT
EEESDSDYEQNSENDDESEINPSNSYYNDKALLEAQSVARAKQLRAKFEKWQNNEIEQ
EIKEGRIDVYSQLISNESIESAKAIREFENMKKSETAMENPSKTQIKRFV"
join(18584. 18839,18906. 1916),25083. 25226,25280. 26049,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="FLYBASE:FBan0017467"
/db_xref="FLYBASE:FBan0022341"
complement(join(7848. .7850,7901. .7982,8045. .8187,
9658. .10140,10199. .10297))
/gene="CG17467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9658. .10140,10
/gene="CG17467"
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ASEKELEKNLPTFKDNDFIKQKVKLDIGKEAKDKLMDTLSNDVDLLTKLHIMDYSLLV
GVHDCVRAEBEALQODNILTVGRSENSESEBCDSGERFATNTTGIKIRELMYILNCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="FLYBASE:FBgn0022341" complement(<7685. .>10336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(7685. .7850,7901. .7982,8045. .8187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FLYBASE:FBgn0039924"
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/db_xref="GI:10728139"
/db_xref="FLYBASE:FBgn0002521"
/protein_id="AAF59378.1"
/db_xref="GI:7304348"
                                                                                                                                                       /note="pho gene product; Nucleotide sequence of the Celera
sequence differs from the published sequence for this
transcript"
                                                                                                                                                                                                                                                                                                                   /map="102E3-102E5"
/db_xref="FLYBASE:FBan0017743"
/db_xref="FLYBASE:FBan002521"
/db_xref="FLYBASE:FBan0002521"
/db_1(19069: .19163,25083: .25226,25280: .26049,26111: .26402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <18584. .>27740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the published sequence for this transcript."
/product="CT39329"
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/gene="pho"
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FGVDDVDYRESLTRSQPIQIDSSGKSGAQFYQSYDKFFI I KSLTSEEI ERMHAFLKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="FLYBASE:FBan0017471"
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join(3750. .3887,3945. .4042,4116. .4365,4417. .4547,
4611. .4779,6348. .6499,7372. .7501,7555. .7671)
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                                                                                                                                                                                                                                                      27005 . .27124,27178 . .27325)

'gene="pho"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="pho"
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                                                                                                                            'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="FLYBASE:FBgn0002521"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         map="102E1-102E3"
                                                                                           db_xref="FLYBASE:FBan0017743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="FLYBASE:FBan0017743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Nucleotide sequence of the Celera sequence differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="FLYBASE:FBan0017467"
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translation="MAYERFGIILQSEQYDEDIGNTKVNQKMNEGKGNHYDLHRKNAF"

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Query Match
Best Local
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GTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATA 264
                                                                                                                                                                                                                                                                                                                                                                                                          CTTGACAAATCATGGATAGCTGTTCTACTAATAATAGGTCATATTGCAATGTGGTATCTA 444
                                                                                                   TTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATA 384
                                                                                                                                                                                                     TCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACAT 324
                                                                                                                                                                                                                                                                                                         GTTAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGGATACTAATT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCTCTATGTCGTCATGGTTTAATATATGGAATAATGCATTAAGCGATCTAGGACATGCT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194;
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/db_xref="FLYBASE:FBgn0039925"
complement (<33838. .>35332)
/gene="CG17461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNMNSTKNVQIIDLGRNCKASFKTNNSILTKPNFPLIQSKEEVQLQARSRIDLIKRSL
IGGERIHDFELKEKHMARKYAAQRHLSAIAIALSRVKCEDRDLLQGHYATITQEIDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVSVPTLTTQPVVNANQCYDWLHFGNKNRVTAATLMNKNSSRSHTIFTITLEQSPFLN
SIGSDAFGGICRGKLSLVDLAGSERQRKTGAQGDRLKEASQINLSLSALGNVISSLVD
GKAKHVPFRDSKLTRLLQYYFNKDSLGGNTKTLMISCISPTDIHYDETISTLRYASRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="FLYBASE:FBan0017461"
/db_xref="FLYBASE:FBgn0039925"
complement(join(33838...34674,34722.
/gene="CG17461"
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CGKAFVESSKLKRHQLVHTGEKPFQCTFEGCGKRFSLDFNLRTHVRIHTGDRPFVCPF
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NQETSKVLTNSLSKNDINTEESGVVDKNSPFLTIGTILINSKGSKRWEGKLVHIKTM
KQETSKVTMAASGISDDEYSGSDQIVGASDLIKGKEEFGIDGFTSQQNKEYGKMESKFI
EGEFSVTMMAASGISDDEYSGSDQIVGASDLIKGKEEFGILGFTSQQNKEYGKMESKFI
NAQTLEMPHPISSVQIMDHLIKERGNLSQENNISERILSKTTLSFEEPIILLPDSSSIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(50956. .51220,52591.
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/db_xref="FLYBASE:FBqn0039925"
/protein_id="NAF59380.1"
/db_xref="GI:7304350"
/translation="NTTNVRYLALVTYLEIYNERIRDLLNKNENTNVINHFLKELPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVTENHVPFVVYAD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDYIRKCKEKIKMLEMEVSDLNSEFQLDREDYLDEIRNLGRQVKFHQQLFLKFSSNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNISNKPKINEDPKDARLRQYQNEILYLKRMLQESQQIINKNNDPNKIIKSPLKIIQH
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/gene="CG17461"
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Pred. No. 2
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RESULT AC014617 B 8 B 8

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                                                                                                                                                                                                                                                                                                                                  265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                               TTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATA 384
                                                                                                                                                                                                                                                                                                  TCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACAT
                                                                                                                                                                                                                                                                                                                                                              GTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATA 264
                                                                                                                                                                                                                                         PROGRESS
AL513530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD, USA
This sequence was identified as CDM:10212914 by
For further information on this sequence e-mail
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                             HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyce Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 21595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                          AL513530.2 GI:12750914
                                                                                       Homo sapiens chromosome 6
                                                                                                      AL513530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the finished sequence as soon as it is the accession number will be preserved.
                             HTGS_PHASE1
sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Venter, J.C.
                                                                       ***, 16 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster'
/db_xref="taxon:7227"
3538 c 3704 g 7250 t
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                                                                                       *** SEQUENCING
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to fly@celera.com.
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TITLE
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                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 192242; sum-of-contigs
Insert size: 175186; 1.1% error; agarose-fp
Quality coverage: 5.03x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: plasmid; 108752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 189015 bases at least Q40 Consensus quality: 191018 bases at least Q30 Consensus quality: 191870 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requests: clonerequest@sanger.ac.uk
On Feb 12, 2001 this sequence version replaced gi:12743866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: bA447M22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coverage: 5.74x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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/db_xref="taxon:9606"
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48345: contig of 4090 bp in length
4845: gap of 100 bp
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129937: contig of 6062 bp
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123775: contig of
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193742: cont
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88503: contig of 40058 bp in length
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20: contig of 13454 bp in length
123: gap of 100 bp
27549: contig of 5426 bp in length
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59: gap of 100 bp
44155: contig of 8396 bp in length
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4: gap of 100 bp
8469: contig of 2875 bp in length
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fragment_chain:3"
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Chang, W.T., Newell, P.C. and Gross, J.D.
Identification of the cell fate gene stalky
Cell 87 (3), 471-481 (1996)
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/protein_id="AAB36702.1"
/db_xref="GI:1685115"
                                                                                                                                                                                                                 /note="a knock-out of this gene gives the phenotype of loss of the ability to complete spore formation leading the formation of a fruiting body containing only stalk
                                                                                                                                                                                                                                                                                                     493
                                                                                                                                                                                                        cells"
                                                                                                                                                                                                                                                                                                                          /organism="Dictyostelium/strain="NC4"
/db_xref="taxon:44689"
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                                                                                                                                                                                                                                                          /gene="stkA"
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Sequencing vector: M13; 49%
Sequencing vector: M13; 49%
Sequencing vector: plasmid; 51%
Chemistry: Dye-primer ET; 37% of reads
Chemistry: Dye-terminator Big Dye; 63%
                                                                                                                                                                                               Direct Submission
Submitted (25-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Nov 30, 2000 this sequence version replaced gi:11323453.
                                                                       Center project name: H_NH0550H09
                                                                                                                                Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                             2 (bases 1 to 179401)
Waterston, R.H.
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Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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NAPLLORLIHVVENQLLEPNELSSIREDIDIMKNDLILEKKKALAQLKDLKOKANDV
QILKANIEKGSNQRSNETKSFITELKQEIDKRINQXTHIYIPPDHHLVPSSTNYLSID
SLQNSSSSNNYCTIHNSNNNNNNNNNNKRSLVNLSPELIHSPLKKPMVGGYRDEQGM
KHFSIDGDNLSLPSIS"
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   of reads
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                                                                                                                                                       CAAATCATGGATAGCTGTTCTACTAATAATAGGTCATATTGCAATGTGGTATCTACA 446
                                                                                                                                                                                              AGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCAT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTAT 209
                                                                                                                                                                                                                                   AGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATACTTGA 389
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Insert size: 174000; sum-of-contigs
Quality coverage: 6.28 in Q20 bases; agarose-fp
Quality coverage: 6.19 in Q20 bases; sum-of-contigs
AC021920 84346 bp DNA
Homo sapiens clone RP11-23J11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It curren consists of 3 contigs. The true order of the pieces
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75349. .179401
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/db_xref="taxon:9606"
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34893. .75248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vasailie, W. H. Viel, R. V. A. Wi, Y. Warmen, D. V. W. J.,
Tirrell, A., Vasailie, W. H. Viel, R. V. A. Wi, Y. Warmen, D. V. W. J.,
Talamas, J., Tesfaye, S., Theodore, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6730861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens, clone RP11-23J11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This record contains 79 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      will be sequenced to completion. In the event the the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            However,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project Information Center project name: L4379 Center clone name: 23_J_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                              2117 3116: contig of 1000 bp in length 3117 3216: gap of 1000 bp in length 3217 4132: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                     935 1034: gap of
1035 2016: cor
                                                                                                                                                                                                                                                        4133 4232:
                                                                7376: gap o
                                                                                                                    2 6351: gap c
2 7276:
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                  8461: gap
9418:
                                                                                                                                                            100 bp 100 bp 1232: contig of 916 bp 1232: gap of 100 bp 1516: contig of 944 bp 11276: gap of 100 bn 151.
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                                                                                                                                                                                                                                                                                                                       100 bp
100 bp
116: gap of 100'
316: contig of 982 k
                                                                                                                                                                                                                                                                                                                                                                                                                                      934: contig of 934 bp
                                        contig of 925 1
o of 100 bp
contig of 985 1
o of 100 bp
                                                                                                                                               contig of 975
of 100 br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nusbaum, C. and Lander, E.
1 of 957 h
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                     bp in length
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0622 11585: contig of 964 1586 11685: gap of 100 b 1686 12674: contig of 989

bp in length

bp in lengt

bp in length

10621: 9518:

gap of

1585

gap of 0521: contig

of.

) bp 1003 bp in length

12774: gap of 100 k 13775: contig of 1001

866 15965:

17044:

gap of

17985:

76 13875: gap of 10 76 14783: contig of 9 76 14783: gap of 19 14883: gap of 19 84 15865: gap of 10 66 15965: gap of 10

f 982 bp 100 bp

bp in ni dq

length length

908

986 18085:

gap of contig of

100 bp

bp in length

bp in bp in length

length

07 20206:

21276:

276: gap of 10 22256: contly of 9 1356: gap of 1 23336: contly of 9 1436: gap of 1 24405: contly of 9

100 bp

bp in length bp in length bp in length

969 980 980

bp in length

bp in

length

86 19048: contig of 963 bp 49 19148: gap of 100 bp 49 20106: contig of 958 bp 97 20206: gap of 100 bp 97 21176: contig of 970 bp

100 bp 1958 bp in length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                       61163 TGTATAAGCATTCTCTTTTCTCTGTAGTCTTGCCAGTTATCTATTGTTTTATGACTATTT 61222
                                                                                                                61223 AAAAAATAGTCATTCCGACTTGTGTGAGATTGTATCTCATTGTGGTTTTGATTTACATTT
                                                                                                                                                                                                                                                                            170 TCAATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTATAAGTTGGTTTAAGAAATCTTT 229
                                                 290 TAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGTTTTTCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                      110 TATGGAATAATGCATTAAGCGATCTAGGACATGCTGTTAAAAAGCAGTGTTGCTCCAATAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 8.18;
Local Similarity 46.28;
es 148; Conservative
TTTGAGAAGTATCTCCTGATGTTATTTGATCGTTTTTAATAGAATTATTTGTTTTTTTCT 61402
                                                                                                                                                            ATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAACTTAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 59929: yar and yar are also be seen to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53273 53372: gap of 100 bp
53373 54370: contig of 998 bp
54371 54470: gap of 100 bp
54471 55469: contig of 999 bp
55470 55569: gap of 100 bp
55570 55544: contig of 975 bp
56545 56644: gap of 100 bp
56645 57668: contig of 1024 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73655 73754: gap of 100 bp
73755 74680: contig of 926 bp
74681 74780: gap of 100 bp
74781 75782: contig of 1002 b
75783 75882: gap of 100 bp
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4 52181: contig of 9
2 52281: gap of 10
53272: contig of 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58828:
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49030: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50105:
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59829: contig of 1001 l
9929: gap of 100 bp
60913: contig of 984 b
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3654: contig of 925
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28: contig of 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44.8; DE Pred. No. 7.9; 0; Mismatches
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f 984 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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28696 28795: 27616 27715:

158 25557:

26641:

244UD: COUNTY TO BE TO SEE TO

100 bp f 974 bp in length

bp in length

06 24505: 37 23436: 57 22356:

6160 36259:

100 bp

bp in length

997 965

bp in

length

35162: 34060: 2886 32985:

1938: gap of 10
32885: contig of 9
2885: gap of 10
33960: contig of 9
4060: gap of 10
35062: contig of 10
35162: gap of 10
5162: gap of 10

100 bp f 975 bp in length 100 bp

1002 bp in length

839 31938:

100 bp f 947 bj

bp in length bp in length

87 30886:

96 28795: gap of 106 29720: contig of 1192820: gap of 11921 30786: contig of 119388: contig of 1193888: contig of 119388: contig of 119388

100 bp £ 966 bp in length

925

bp in length

bp in length

100 bp

952

3160 36259; gap of 10 37224; contig of 17 7225 37324; gap of 11 7325 38293; contig of 18 3294 38393; gap of 10 3294 38397; contig of 19

100 bp of 969 bp in 1 100 bp of 984 bp in

length length

4690 44789:

12653: gap of 100 bp in 1
43612: contig of 959 bp in 1
43712: gap of 100 bp in 1
14789: contig of 977 bp in 1
14789: gap of 100 bp in 1
45718: contig of 929 bp in 1
45818: gap of 100 bp 1
45818: gap of 100 bp 1
45818: gap of 100 bp 1

43712: 42653: 41578: 40510: 39477

0510: gap of 1 41478: contig of 1578: gap of 1 42553: contig of

100 bp f 968 bp

bp in

100 bp f 975 bp in

length length

length

177: gap of 100 bp 40410: contig of 933 bp in

45818:

46847: gap of 47815: contig of 47915: gap of

100 bp

in

length

length

	9	i.	
/evidence=not_experimental 4115 4261	gene	/db_xref="taxon:4907" /note="synonym:Hansenula wingei"	
D II		/organelle="mitochondrion" /strain="21"	
/evidence=not_experimental	PYON		source
<pre>/cons_spiice=(5.site:no, 3.site:no) /number=1</pre>		(E-mail: NJ1302*0FWHIKOK. BINE1, Tel: 0024-24-7433, Edx: 0024-24-0734) Location/Qualifiers	FEATURES
="COX1"		1-3-1 Kagamiyama, Higashi-Hiroshima, Hiroshima 739, Japan	
NSYVKENSSRTTKFNKLMLCSKYYDLINIKAWLIENKNENSKE" 1964 2962	intron	Submitted (U/-JUN-1994) to the DUBJ/EMBL/GenBank databases. Kazuo Yoshida, Hiroshima University, Department of Biological Science;	JOOKNAL
NYYFKNNYPQLTISVSNKKYIDLKPFMDIFGGNIYYDKSNNGCYKWSIQSKTDILFFI		mission	TITLE
AGLIDGDGYLGVSKAGYTSCEITVALEDEKALRQIQNKFGGSIKIRSGIKAIRYRLHN KFGMTKLINAINGNTBNTKBLDOLHKVCSTINIDITEDINITINNSWETGEEDADGT		6 (bases 1 to 27694) Yoshida, K.	REFERENCE
YKLAILVKILIYYNNNQQITNNMIKIIKRYKSYLVGISETIRKNSDLDKKDIKFNQWL		Genes Genet. Syst. (1996) In press	JOURNAL
/db_xref="GI:11036338"		complete nucleotide sequence of mitochondrial small subunit rRNA in	
/protein_id="BAA06564.2"		The secondary structure and phylogenetic relationship deduced from	TITLE
<pre>/evidence=not_experimental /product="intronic OPE"</pre>	•	5 (sites) Okamoto.K. Sekito.T. and Yoshida.K	AUTHORS
/transl_table=4		96132035	MEDLINE
/note="no ATG start codon"		Clone bank of the mitochondrial genome of yeast Hansenula wingei	TITLE
♬.	C	Sekito, T., Okamoto, K., Kitano, H. and Yoshida, K.	AUTHORS
SIKSASIEFILNSPPALHSFNTPAVQS" <1964	CDS	4 (sites)	REFERENCE
WNYVSSIGSVIAIISLALFIYIIYDQLINGLTNKIDNKSVVYSKAPDFVESNTIFANN		Curr. Genet. 28 (1), 39-53 (1995)	JOURNAL MEDI THE
GYYYWSPQILGLYFNERLAQIQFWLIFVGANVIFMPMHFLGLQGMPRRIPDYPDAYAG		new characteristics of yeast mitochondria	
AMASTAFLGFLYWSHHMYIYGLDADTRAYFTSSTMYIAYPTGIKIFSWLATLYGGSIR LAVPMLYAIAFLFLFTIGGLTGVALANASI,DVAFHDTYYVVGHFHYVLSMGAIFSLFA		The complete mitochondrial DNA sequence of Hansenula wingei reveals	TITLE
TSFFEVAGGGDPVLYQHLFWFFGHPEVYILIVPGFGIISHIVSTYSKKPVFGEISMVY		1 to 27694)	REFERENCE
LGAINFIATSYNMRTNGMSYSKMPLFVWAIIITAVMLLLSLPVLTAGVTMLLMDRNFN		Nucleic Acids Symp. Ser. 31, 233-234 (1994)	JOURNAL
SEWILPPALVCLVASTLIESWAGTGWTIYPPLSGIOAHSSPSVDLGIFAIHLTSISSL			
/translation="MYIQRWLYSTNAKDIAILYFIFAIFSGVIGSTMSLIIRLELAAP GNOTLHGNHOLFNVLVVGHALLMTFFLVMDGLVGGFGNYMLDLLTGASDMGFARLNNT		Yeast Hansenula wingei mitochondria genome's complete DNA seguence	TITLE
/db_xref="GI:11036337"			REFERENCE
/protein_id="BAA06563.2"		International Botanical Congress, 503-504 (1993)	JOURNAL
/evidence=not_experimental		The structure and organization of mitochondrial genome in Hansenula winger	BTILLE
/transl_table=4		nida, K.	AUTHORS
/codon_start=1)	REFERENCE
join(12411963,29633847)	CDS	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;	
/evidence=not_experimental		Mitochondrion Pichia canadensis	z
/gene="COX1" /number=1		Pichia canadensis (strain:21) mitochondrion DNA.	SOURCE
1241. 1963	exon	RNA-Arg-2; transfer RNA-Leul; transfer RNA-Met3; transfer RNA-Ser1;	
/gene="COX1"	9	tRNA-Trp; tRNA-Tyr; tRNA-Val; transfer RNA-Arg-1; transfer	
/gene="trna-c" 1241 3847	gene	trna-Tle: trna-Leu2: trna-Lys; trna-Phe: trna-Pro: trna-Thr:	
832 903	gene	ribosomal RNA; small subunit ribosomal RNA; tRNA-Ala; tRNA-Asn;	
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/note="anticodon=uuc"		N PICNIA CANAGENSIS MITOCHONGITAL DNA, COMPLETE SEQUENCE. D31785	ACCESSION
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/gene="tkNA-1"" 714785	tRNA		a
	gene	~	RESULT 13
/product="transfer RNA-Thr"			
/note="anticodon=ugu"			61463
/gene="trnA-T"	CRNA	TACTAATAATAGGTCATATT 429	Qy 410
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/gene="LSU"	exon		
י אחר ה	מכאס	TATCAATAATAGCATATTTCATAGCTATATCAATACTTGACAAATCATGGATAGCTGTTC 409	Oy 350

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Matches
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Best Local
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                                                                     Conservative
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LAPLLVLIELLSYSARAISLGLRLSANTLSGHLLMVILGGLVFNLMSVSIVTFVLGFI
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                                                                                 8.0%;
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                                                               Score 44.4; D
Pred. No. 10;
0; Mismatches
                                                                 0;
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REFERENCE
AUTHORS
TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCT
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                                                                                                                   Chemistry: Dye-primer ET; 93% of reads Chemistry: Dye-terminator Big Dye; 7% of read Chemistry: Dye-terminator Big Dye; 7% of read Assembly program: Phrap; version 0, 990319 Consensus quality: 172750 bases at least Q40 Consensus quality: 176629 bases at least Q30 Consensus quality: 178424 bases at least Q20 Insert size: 191000; agarose-fp Insert size: 194940; sum-of-contigs
                                                                             Quality coverage: 4.41 in Q20 bases; agarose-fp Quality coverage: 4.66 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _{\rm M}^{\rm O}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                        Sequencing vector: M13; 95% Sequencing vector: plasmid; 5%
                                                                                                                                                                                                                                                                                                                                 Center project name: H_NH0487E01
                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 1 clone RP11-487E1, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                           Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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     NOTE: This is a 'working consists of 23 contigs. The is not known and their or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aug 26,
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                                                                                                                                                                                                                                                                                                               Summary Statistics
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         order
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                         note="assembly_name:Contig18"
                                                                                                                                                                                                                'note="assembly_name:Contig16"
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y of 4775
f unknown
y of 4504
f unknown
f unknown
t of 4386
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Human BAC clone CTB-167B5
AC003991
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Mammalia; Eutheria;
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51209. .55594
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1730. .46504
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 8.8;
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DB 71; 126;

Length 185926;

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04-FEB-2000

2206 others

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JOURNAL REFERENCE.
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Murray,J., Rohlfing,T. and Antoniou,B.
The sequence of H. sapiens BAC clone CTB-167B5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send mailto:egreen@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of CTB-167B5:
actual end of this clone is at base position 118313 of CTB-167B5.
                                                                                                                                                                                                                                                                                                                                       Clone CTB-167B5 is from the first release of the human BAC library CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-FEB-2000)
University, 4444 Forest
4 (bases 1 to 118313)
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                                                                                                                                                               This clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
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It may be shorter because we only sequence overlapping
sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                     pBeloBAC11
    /clone_lib="CITB-978SK-B"
/map="7q21"
                                           /clone="CTB-167B5"
                                                                /db_xref="taxon:9606"
/chromosome="7"
                                                                                                   /organism="Homo sapiens"
                                                                                                                                          Location/Qualifiers
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Park Avenue, St. Louis,
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Missouri 63108,
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20347. .20
                      /rpt_f.
21425.
                                                            /rpt_family="Alu"
21158. .21226
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18644.
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17199
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11353.
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/gene="SRI"
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4701. .4865
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686. .832
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527. .626
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15947. .16238
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1359. .1503
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1073. .1117
/rpt_family="Alu"
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nutlidrug-resistant cells"
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11. .19157
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Db 100958 G 100958
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                                                                                                                                                                                                                                                                                                                                     Query Match 8.0%; Score 44.2; DB 85; Length 118313; Best Local Similarity 49.0%; Pred. No. 10; Matches 118; Conservative 0; Mismatches 123; Indels 0; Gaps
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                                                                                   212 TTGGTTTAAGAAAICTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGG 271
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                                 272 G 272
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37394. .37548
/rpt_family="MaLR"
37657. .38131*
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/rpt_family="MER81"
21910. .22079
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36634. .37363
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30548. .30650
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29217. .29523
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8961. .29023
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2715. .23122
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6564<sub>.</sub> .26742
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3. .32121
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Search completed: May 30, 2001, 23:07:52

Job time: 4726 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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Sequence encoding
Human IL-1ra BAC c
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                                                                                         Plasmodium falcipa
Nucleic acid seque
Upstream sequence
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ALIGNMENTS

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Reid J, F
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disease resistance; feedstuff; ss.
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                                  , Kosmotka A, Link S, Maffia AM, M
Robertson DE, Swanson RV, Warren PV;
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                                                                               Murphy D;
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This DNA sequence codes for thermostable esterase F1-12IC (W23069)

Cof Staphylothermus marinus F1, a thermophilic sulphur archaea that grows optimally at 85 deg C and pH 6.5. It can be amplified from a pBluescript vector by PCR (see T79299-300). Claimed, newly identified polynucleotides (T79321-30) encoding esterases (W23069-207, W23088) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
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Best Local Sim
Matches 555;
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P-PSDB; W23069.
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                                                                      CCCGAGTTATTAGCGGTATTCTCGTTTTTACCATTCTATATAAGACAGTATTTTAAATCA
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                                              cccgagttattagcggtattctcgtttttaccattctatataagacagtattttaaatca
                                                                                                                                                ggtcatattgcaatgtggtatctacactttgcttcagagattccgagaggtgctgctatt
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31 ATGATAATATTTATTCTCAGCTTTTCCTTTCCCATTAACAATGATCGCATTAGCTATCTCT

Query Match Best Local Similarity

7.68;

Score 42.2; DI Pred. No. 0.17, 0; Mismatches

DB , 17; 218;

Length

Indels

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Conservative

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The present invention describes proteins and their fragments (I) encoded CD by chromosome 2 of the human malarial parasite, Plasmodium falciparum. CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against P. falciparum infection comprising the sequences of (I), are CC useful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum (CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the CC subsequent identification of proteins encoded by it will help to expand CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito CC parts of the world, and there is a pressing need for vaccines and new CC drugs. A70078 to A70287 and B18144 to B18352 represent nucleotide and CC protein sequences given in the present invention, but which are not expectifically mentioned within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF/) HOFFMAN (CARU/) CARUCCI I (GARD/) GARDNER I (VENT/) VENTER J
                                                                                                                                                                                                                                                                                                                                                                                                           Proteins encoded by chromosome 2 of the human plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 470-471; 577pp; English.
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 Sequence
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CARUCCI D.
GARDNER M.
VENTER J C.
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 1641 A; 269 C;
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vaccines
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and in the
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore,
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                                                                                                                                                               Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial
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                                                                                                                                                 diagnosis of P.falciparum infection
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                                                                                                                        Disclosure; Page 548-549;
                                                                                                                                                                                                                                                                   (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
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                                                                                                                                                                                                                               Carucci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             protozoacide;
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L vaccines
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and in the
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                                                                                      (HOFF/)
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                            Hoffman
                                                                                                                                  05-NOV-1998;
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                                                                                                                                                                                                                                                     Plasmodium falciparum
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antimalarial; malaria;
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                                                          (VENT/)
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                                                                         (GARD/)
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les 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAACAAAATTATGAATATCCATAAAAAATATAATGCCAGAACGATTTAATATTAACATAT 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAGCGATCTAGGACATGCTGTTAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTATGAGGTTTTAAAAAATCGTTAATTATAATCATTCCGTTTTTTGTTCCTATAACAA 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTCATAGCTATATCAATACTTGACAAATCATGGATAGCTGTTCTACTAATAAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCAT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACG 304
                                                                      HOFFMAN S. CARUCCI D. GARDNER M.
                            s
                                                        VENTER J C.
                            Carucci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                  98US-0107131
                                                                                                                                                                99WO-US26796
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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46.1%;
                            D,
                                                                                                                                                                                                                                                                                                                                                                                                                            3927
                                                                                                                                                                                                                                                                                   chromosome 2;
protozoacide;
                            Gardner
                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                            Z,
                            Venter
                                                                                                                                                                                                                                                                                    infection;
                                                                                                                                                                                                                                                                                                 human malaria parasite;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159;
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                                                                                                                                                                                                                                                                                      insecticide;
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                                                                                                                                                                                                                                                                                                                                ID NO: 234
                                                                                                                                                                                                                                                                                    vaccine;
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WPI; 2000-365347/31

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention environment of the present invention and arial parasite, Plasmodium falciparum.

CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) or vaccines against p. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against p. falciparum infection. (I) and polyclonal antisera or a monoclonal contribody raised to immunogens comprising the sequences of (I), are constituted in the detection of infection with p. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) con aid the identification of drugs to treat or prevent p. falciparum infection, or they can be used to identify drug resistance in comprisition.

CC p. falciparum. Sequencing of the plasmodium chromosome 2 and the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, and provide new targets for complexity of the parasite biology, and provide new targets for complexity of the parasite biology, and provide new targets for complexity of the parasite biology, and provide new targets for complexity of the parasite biology, and provide new targets for complexity of the parasite biology, and provide new targets for complexity of the world, and there is a pressing need for vaccines and new complexity of the world, and there is a pressing need for vaccines and new complexity of the world, and there is a pressing need for vaccines and new complexity of the parasite in the present invention, but which are not conserved.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 163;
                   05-OCT-1999
                                                             x99599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines
                                                                                                     X99599 standard; DNA; 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3927 BP; 1786 A; 198 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 458-459; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis of P.falciparum
                                                                                                                                                                                                              407
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                                                                                                                                                                                                                                                                                                467
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                                                                                                                                                                                                                                                                                                                                                                                                                             292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 TTTTCTTTCCCATTAACAATGATCGCATTAGCTATCTCTATGTCGTCATGGTTTAATATA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes proteins and
                                                                                                                                                                                                                                                                                                                                                                                                          GGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGTTTTTCTTA
                                                                                                                                                                                                            ACATTTTTA 399
                                                                                                                                                                                                                                                                                                                                     TCAATAATAGCATATTTCATAGCTATATCAATACTTGACAAATCATGGATAGCTGTTCTA 411
                                                                                                                                                                                                                                                                                                                                                                               AAATGTTCCATATGTGAATCATTTACAAAAATGTTACTATTGTTAGAATGTATTACATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTGAAAGAAGCTAAAATTAGTTTGATCTATTTTAAAAAATTCATCTGTAATATCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGTATGTTTCATTAACTCTTCTTCATTTACGTTTTTCTTATTTTCAAAAGATGTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTATAGTTGGTTTAAGAAATCTTTAT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAATAATGCATTAAGCGATCTAGGACATGCTGTTAAAAGCAGTGTTGCTCCAATATTC 171
                                                                                                                                                                                                                                                                                                TTATTATTATTATTATTATTATTACCATTTGATGGATAAATATTATAACTTGTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAACTTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1260 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3927;
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and in the
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270 GGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCT

gattgaattaaacttattaccatgatattcaaaatcaattagaaattgttcgtatttaat

402 329 210 AGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCAT

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                                                                                                                                                                                                                                                                                            The present invention provides methods for the detection and diagnosis of Ureaplasma urealyticum infection. It provides novel genes (X99501-681) that can be used as a source of primers and probes for the detection and/or quantification of U. urealyticum in a biological sample. The probes of that can be used in the method of the invention by forming target:probe complex is computementary to a region selected from one of the 181 curealyticum is an opportunistic nucleic acid sequences (X99501-681). U. urealyticum is an opportunistic pathogen of the human urogenital tract that is a significant cause of adverse pregnancy outcome, neonatal disease, and suppurative arthritis. As the infections are commonly asymptomatic, it is important to have specific and sensitive methods for detecting their presence in a patient. Also, as the pathogen has no current antibiotic directed specifically against it, it would be advantageous to isolate and detect gene sequences which are unique to it, and utilise these as a basis for diagnosis of U. urealyticum infection as well as to develop new and improved drug therapies. The present invention provides such novel polynucleotide
                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cassell GH, '
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suppurative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ureaplasma urealyticum; nucleic acid detection; infection; pathogen;
human urogenital tract; pregnancy; neonatal disease; drug therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UABR-) UAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequence from U. urealyticum.
                                                              166 aatattctcataatt---aatttgtgttttttacattaaaaaaatcatcaaaaaccagaaag
                                 150 AAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTAT
                                                                                                                                   106 taaaataattggtgtgttaaatttaatattttcatcttctaaaattgattttaataaatt 165
                                                                                                 90 TATGTCGTCATGGTTTAATATATGGAATAATGCATTAAGCGATCTAGGACATGCTGTTAA 149
                                                                                                                                                        30 TATGATAATATTTATTCTCAGCTTTTCTTTCCCATTAACAATGATCGCATTAGCTATCTC 89
aattaattgtttactaatattaatgttattagtatcgaattgttctaaatccatattatt
                                                                                                                                                                                                          183;
                                                                                                                                                                                                                                                                                          615 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis; ss.
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen EY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0073189
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                                                                                                                                                                                                                                                                                          227 A; 64 C;
                                                                                                                                                                                                                       7.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glass
                                                                                                                                                                                                       Score 39.2; DB Pred. No. 0.62; 0; Mismatches 2
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                                                                                                                                                                                                                                                                                          G; 264 T; 0 other
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                                                                                                                                                                                                                                        DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes,
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                                                                   Query Match
Best Local
                                                 Matches
                                                                                                                                                                                                         Carboxylate synthase (ACC) gene and incorporates a promoter sequence. The invention provides a new recombinant polynucleotide that comprises a promoter sequence which is an inducible promoter obtainable from apple or a functional portion of that promoter. The promoter is most preferably the Apple beta Galactosidase (ABGI) promoter or the ACC synthase promoter and is activated in response to tissue specific agents (especially agents specific to ripening fruits). A host plant cell transformed with a replication vector comprising one of the promoters and a replication vector comprising one of the promoters and a replication of the vector can be used in a method to produce transgenic apple plants. The transgenic plants can be cultivated to produce apples having a modified phenotype. The invention may be used to induce protein expression in specific plant tissue, for example in order to control fruit ripening, or to introduce protective proteins. The invention may also be used to isolate other ripening.
                                                                                                                                                              specific promoters or transcription factors, or in genome mapping. A probe comprising one of the promoter sequences can be used to separate a transcription factor from fruit cells.
                                                                                                                                  Sequence 5391 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This represents the upstream region of the 1-AminoCyclopropane-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New inducible plant promoters from apple - useful to construct vectors for tissue-specific expression of transgenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-583199/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gittins JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UKAG-) UK MIN FISHERIES & FOOD
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09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apple beta galactosidase; ABG1; ACC; promoter; ripening; fruit; apple; 1-AminoCyclopropane-1-Carboxylate synthase; transgenic; genome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Upstream sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V71729 standard;
195 GATACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGGTTAAAGGATC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attatcaatggttttgtataaattagcaaaagccttgttagtaaagtgatcaatacttga
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                                                   l Similarity
98; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 5; 52pp; English.
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hiles ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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97GB-0007193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                  1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the ACC synthase gene.
                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS
                                                                                                                                  A; 929 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    James DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                   0
                                                Score 39.2; Di
Pred. No. 1;
0; Mismatches
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                                                                                                                                  855 G;
                                                                                                                                  1792 T; 0 other;
                                                                                  DB
                                                 98;
                                                                                  19;
                                                 Indels
                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome mapping;
                                                                                  5391;
                                                 0;
                                                Gaps
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RESULT
V71738
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                           This represents the upstream region of the 1-AminoCyclopropane-1-
CC Carboxylate synthase (ACC) gene and incorporates a promoter sequence.
CC The invention provides a new recombinant polynucleotide that comprises a
CC promoter sequence which is an inducible promoter obtainable from apple or
CC a functional portion of that promoter. The promoter is most preferably
CC the Apple beta Galactosidase (ABG) promoter or the ACC synthase promoter
CC and is activated in response to tissue specific agents (especially agents
CC replication vector comprising one of the polynucleotides and a
CC replication vector comprising one of the polynucleotides and a
CC replication of the vector can be used
CC in a method to produce transgenic apple plants. The transgenic plants can
CC be cultivated to produce transgenic apple plants. The transgenic plants can
CC cultivated to produce apples having a modified phenotype. The
CC invention may be used to induce protein expression in specific plant
CC tissue, for example in order to control fruit ripening, or to introduce
CC protective proteins. The invention may also be used to isolate other
CC uniquently a probe comprising one of the promoter sequences can be used
CC to separate a transcription factor from fruit cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1997;
09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1621
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                              New inducible plant promoters from apple - useful to vectors for tissue-specific expression of transgenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gittins JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apple beta galactosidase; ABG1; ACC; promoter; ripening; fruit; apple; 1-AminoCyclopropane-1-Carboxylate synthase; transgenic; genome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Upstream sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V71738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1741 gatgtcaacatgtggc 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UKAG-) UK MIN FISHERIES & FOOD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1561 gttaattttttttttatgttgtttaatgttacttaatgttatttaatgttgtttaatattg 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATATCAATACTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tttaatgttgtttcatgttacttaatgtcacttaatgttgtttaatgacttaggaagtta 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTAATCATATCCATGGGTGTATTTCTTAACCTTAATAGGGGTTTTTCGACGAAGTATATGG 314
                                                                                                                                                                                                                                                                                                                                                                                             Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97GB-0011233.
97GB-0007193.
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                                                                                                                                                                                                                                                                                                                                                                                           6; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the ACC synthase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    construct
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Sequence 5407 BP; 1828 A;

930 C;

854 G;

1795 T; 0 other

DB 19;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1741
                                 Barash SC,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1681
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         WPI; 1997-374922/35
                                                                                          05-JAN-1996;
                                                                                                                07-JAN-1997;
                                                                                                                                                              EP786519-A2
                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                        30-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                toxic shock syndrome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V74335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V74335 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 GATACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatgtcaacatgtggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGATACATTTCCTAGTCTCAGTATTGTTTTTTCTTATCAATAATAGCATATTTCATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTAATCATATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98;
                                            Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aureus contig SEQ ID #24.
                                                                                          96US-0009861.
                                                                                                                97EP-0100117
                                                                                                                                                                                                                                             given in
4621..4680
                                                                                                                                                                                                                                                                                                       2821..2880
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 1021..1080
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                                                                                                                                                                                                                                 /*tag-
                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                   SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390
                                            Dillon
                                                                                                                                                                                                 these bases represent a line of missing text in
the sequence listing in the specification. They
                                                                                                                                                                                                                                                      "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                          "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                               the sequence are included
                                                                                                                                                                                     given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ЧB
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                                            Ęď,
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                    the specification
                                            Fannon
                                                                                                                                                                                                to maintain the
                                            MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                            Kunsch
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                                            CA;
                                                                                                                                                                                               nucleotide numbering
                                                                                                                                                                                    this DNA sequence
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likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents one or all acaphylucular readable of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM), or CD-ROM. Homology searches using memory (RAM), read-only memory are functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                         the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 293-296; 3271pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                           readable medium.
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                         QΥ
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                                                                                                                                                                   Query Match
Best Local S
Matches 84
                                                        1354
                                                                                                           1294 tattaatgcagcaattacaccaattactattgttattggaccgcctaaaataccaaacac 1353
1414 tataactgatataatttttaatggtccttttaataacatg
                                                                                                                              263 TATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATAC 322
                                                     agttactagtcctgtgatagcatttctaattaatccaatcttaccgaataacaattggaa 1413
                                                                      ATTTCCTAGTCTCAGTATTGTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAA 382
                          TACTTGACAAATCATGGATAGCTGTTCTACTAATAATAGG
                                                                                                                                                                     84; Conser
                                                                                                                                                                     Conservative
                                                                                                                                                                                 52.5%;
                                                                                                                                                                     0
                                                                                                                                                                                  Score 38.4;
Pred. No. 1
                                                                                                                                                                     Mismatches
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6;
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                          422
                                                                                                                                                                                              Length 5423;
                                                                                                                                                                     0;
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Sequence

5423

BP; 1563 A; 1053 C; 760

G; 1859 T; 188 other;

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GI
                                                                                                                                                                           N60392/c
25-JUL-1985;
11-APR-1985;
11-APR-1985;
                                                                                                                      Sequence
Ag319 of
                                                                        CDS
                           11-APR-1986;
                                                                                             Plasmodium
                                                                                                         Malaria vaccine;
                                                                                                                                          27-JUN-1991
                                                                                                                                                       N60392;
                                       23-OCT-1986
                                                                                                                                                                   N60392 standard; DNA; 1612
                                                                                                                                                                                 9
                                                                                                                      encoding the Asparagine-Rich Protein (ARP) Plasmodium falciparum.
                                                                                           falciparum
                                                                                                                                         (first entry)
85AU-0001640.
85AU-0000108.
85AU-0001008.
                           86WO-AU00092
                                                                        Location/Qualifiers
2..1612
                                                                  /*tag=
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RESULT 10
X02997/c
ID X02997 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                   Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; astma; rheumatoid arthritis; chronic myelogenous leukemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kemp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1612 BP; 831 A; 148 C; 178 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The antigens of the invention are prod. using recombinant DNA techniques. They may be used in vaccine compsns. to stimulate immune response against P.falciparum, the cause of human malar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 8; 52pp; English.
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03-AUG-1998;
                         11-FEB-1999
                                                                                                                                                                                            22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA molecules encoding Plasmodium falciparum antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KEMP/)
                                                 WO9906426-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAATATTCAATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTATAGTTGGTTTAAGAA 223
                                                                           sapiens.
                                                                                                                                                                                                                                                                                                              CCATATTATTATT
                                                                                                                                                                                                                                                                                                                                       CTGTTCTACTAAT 416
                                                                                                                                                                                                                                                                                                                                                                                                                 TATTATTGTTGTTAAGGTTTCTATTTGAAAAGACACCATTATTATTATTATTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the SHARP ARP and MESA antigens
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                                                                                                                                                                    BAC
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                  contiguous DNA sequence 42.
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Mismatches 163; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                      Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibiti interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthrit chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1998;
04-AUG-1997;
   02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IL-1ra BAC contiguous DNA sequence 97.
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                                                                03-AUG-1998;
                                                                                                                                                                                        WO9906426-A1
                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                          11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAATATGATATCTCAAACATCGTTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGTTTTTCTTATC
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98US-0091650
                                                                98WO-US16102
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97US-0054646.
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Pred. No.
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   28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
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                                                                                          03-APR-1998;
                                                                                                                                                                                                                 05-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                            genetic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene expression product cDNA sequence SEQ ID NO:4486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1999
                                                                                                                                                     28-JAN-1999;
                                                                                                                                                                                                                                                                         WO9938972-A2
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression product; diagnosis; therapy;
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98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                                                                                                         colorectal cancer; breast cancer; lung cancer; ss
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53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        typing; profiling;
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                                                                                                                                                                                                                                                                                                                                                                                                                            forensic;
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                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe;
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Sequence 1444 BP; 534 A; 157

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95 G;

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The present invention describes a library of human polynucleotides CC comprising the sequences given in z1253 to z17779. Also described is a CC method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell compected of being cancerous, where the gene product is encoded by one CC of the 5248 polynucleotide sequences given in z12532 to z1779. The CC polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, can be used for raising antibodies for encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and CC arrays for diagnostics (which may be used to determine function of an cenoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to CC identify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC diagnosis, prognosis and management of colorectal cancer, breast cancer, CC centide analogues and antagnists.
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Lamson G, Leshkowitz D,
Stache-Crain B, Sudduth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crkvenjakov R,
Escobedo J, Ga
                                     peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human genes and their expression products which differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-1998;
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Garcia PD, Garcia V, Giese ..,
Kassam A, Kennedy GC, Kita D, Labat 1,
Randazzo F, Reinl
Randazzo F, Reinl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MA;
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RESULT 13
A70199/c
ID A70199
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                    A70199 standard; DNA; 6042
                            07-NOV-2000
                                                                                                                                                          591
                                                                                                                                                                                      383
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 81; Conserv
                                                                                                                                                          TTNTNGNCTNTNGATGNTTGGCNNT 567
                                                                                                                                                                                    TACTTGACAAATCATGGATAGCTGT 407
                                                                                                                                                                                                                                                                          CTNTGATNTGTGTNTANATNNATTANATANTATTNGNNTTNAGANTATGTAGTTTTANAT
                                                                                                                                                                                                                                                                                                     TATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATAC
                                                                                                                                                                                                                                                                                                                                                            TTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAAGGATCTTTAATCA 262
                                                                                                                                                                                                                  ANAGCNNGTNNTTAATNTCNTTTGNNANATAANTAATNGNTGNTTANGTTNCGATTGTNN
                                                                                                                                                                                                                                 ATTTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAA 382
                                                                                                                                                                                                                                                                                                                                 TTATCTTTTGTGNAGTTAGATATNTTANTAGTCNNAGANGTTTNTTANCTNNTTTTNCTN 712
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     39.5%;
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.8; DI
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1444;
                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                     322
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Plasmodium

falciparum chromosome

2 related DNA sequence

SEQ

IJ

NO:332

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The present invention describes proteins and their fragments (I) encoded CC by chromosome 2 of the human malarial parasite, plasmodium falciparum. CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) cc vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC in thody raised to immunogens comprising the sequences of (I), are cuseful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum (CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the CC subsequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC complexity of the parasitic lifecycle, and provide new targets for CC complexity of the parasitic lifecycle, and provide new targets for CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite side resistance to drugs and mosquito cresistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC drugs. A70078 to A70287 and BB8144 to BB8352 represent nucleotide and CC specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CARU/)
(GARD/)
  2255
                                                                                                                                                                                                   2375
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 526-528; 577pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.\,\mathrm{falciparum} infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hof fman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200025728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
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antimalarial; malaria;
                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-365347/31
TGTTCATTATTATTTTATATCTACTATTTTATTTTATATTTT
                                              CATGCTGTTAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCT
                                                                                                                          TTAGCTATCTCTATGTCGTCATGGTTTAATATATGGAATAATGCATTAAGCGATCTAGGA 138
                                                                                                                                                                                                TCTAACATGGAAAAGATATTATATGATTGGATTTTTTCTTTTGTATTATAATATTTAAA
                                                                                                                                                                                                                                                  ) HOFFMAN S.
) CARUCCI D.
) GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ຸນ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VENTER J C
                                                                                                                                                                                                                                                                                                                                                                                                                              6042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carucci D,
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0107131
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                                                                                                                                                                                                                                                                                                                                                                                                                           2818 A; 589
                                                                                                                                                                                                                                                                                                                        6.8%;
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protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gardner M,
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                           ç;
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              627
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                                                                                                                                                                                                                                                                                                                        37.6;
No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                         G;
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infection; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                           2008
                                                                                                                                                                                                                                                                                                                                                ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                           Τ;
                                                                                                                                                                                                                                                                                                 79;
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                                              182
                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                6042;
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RESULT 14 Q94111/c

megakaryocytopoietic cytokine receptor

which may

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21-JAN-1994;
15-FEB-1994;
04-APR-1994;
25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1994;
03-JAN-1994;
      the murine and human ML proteins were aligned, the mouse sequence appeared to have a tetrapeptide deletion between human residues 111-114 which corresponds to the 12 bp deletion at position 618 seen in both human and pig cDNA's (see also Q94109). Additional clones were also examined and one clone was isolated which contained the "missing" tetrapeptide. This sequence is thought to be the full length mML. A further clone was isolated which showed a 116 bp deletion corresponding to bML3 and which was designated mML3 (see also R76166). mML binds to
                                                                                                           (TPO), also known as mpl ligand (mML). This sequence was isolated from a mouse liver cDNA library by screening with a probe comprising the entire human mpl ligand coding region. The first isolated cDNA encoded a protein of 31 amino acids. When the deduced amino acid sequence of the muring and human MI proteins were alleged the mouse component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB2285446-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; thrombopoietin; TPO; mpl ligand; hML; fragment pol; megakaryocytopoietic cytokine receptor; thrombopoietic sic EPO-domain fragment; erythropoietin; hEPO; haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94111 standard; DNA; 1536 BP.
                                                                                                                                                                                             Example 12; Fig 17; 192pp; English.
                                                                                                                                                                                                                                                              WPI; 1995-234018/31.
P-PSDB; R76168.
                                                                                                                                                                                                                                                                                                    Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory thrombocytosis; iron deficiency; EPO; platelet;
red blood cell; progenitor; hML-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            megakaryocyte;
                                                                                                                                                                                                                                  Thrombopoietin polypeptide, ligand for mpl cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic
                                                                                                                                                                   sequence represents a
                                                                                                                                                                                                                                                                                                    DL,
                                                                                                                                                                                                                                                                                                    de Sauvage
                                                                                                                                                                                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                      94US-0223263.
94US-0249376.
94US-0348657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombocytopenia; myeloproliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0348658
94US-0176553
                                                                                                                                                                                                                                                                                                                                                                                               94US-0196689
                                                                                                                                                                                                                                                                                                                                                                                                          9408-0185607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                94GB-0025831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
201.1205
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product=
138. 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Position of frame shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616..731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       531..542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/note= "Position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                       thrombocytopenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMI.
                                                                                                                                                                    genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 bp deletion in mML3,
in 3' end of gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dq
                                                                                                                                                                   encoding murine thrombopoietin
                                                                                                                                                                                                                         related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation
                                                                                                                                                                                                                         diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΩĬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mML2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide;
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DB 15;

Length 1864;

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RESULT 15
Q78892/c
ID Q78892 standard; DNA; 1864 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                   recombinant protein expression and secretion from a filamentous fungus host. The sequence increases the transformation efficiency of the vector. This illustrates the main claims of the patent which provide a vector containing (i) DNA encoding a heterologous polypeptide (chymosin, prochymosin, preprochymosin, Aspergillus niger glucoamylase, Humicola grisea glucoamylase or M. miahei carboxyl protease) and (ii) a secretory signal peptide, and a filamentous fungus (Aspergillus, Trichoderma, Neurospora, podesora fungus (Aspergillus, Trichoderma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1416
                                                                                                                                                                                                                                                                          Vectors and DNA for expressing polypeptide(s) in filamentous fungi - include secretory signal sequences that are native or foreign to heterologous polypeptide(s), such as chymosin or glucoamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transduce a thrombopoietic signal.
                                                                                                                                                                                                 The sequence represents the A. nidulans ANS-1 sequence which is included in the construction of transformation vectors for
                                                                                                                                                                                                                                              Disclosure; Fig 13A-13B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                          WPI; 1994-359750/45
                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1985;
07-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     078892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1536 BP; 413
                             recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                      (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP625577-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector; transformation; protein secretion; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 TGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCATGGATAGCTGTTCTACTAATAATAGGTCATA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGTATTGTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATACTTGACAA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGATCGCTAGCTGCTCTGATGAATATTGCTGATA 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTTTTTTTTTTTTTTTTTTTTAGTGAFTTTCAAATTTATACCGAAAATAGACCA 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                        Endothia, Mucor, Cochiobolus or Pyriclaria, especially A. A. awamori or T. reesei) transformed with the vector for
                                                                                                                                                                                                                                                                                                                                                                       Cullen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nidulans ANS-1 partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     85US-0771374
86US-0882224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86EP-0201751
                           (enzyme)
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52.3%;
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                                                                                                                                                                                                                                                                                                                                                                       Gray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36.6; D
Pred. No. 3.4;
0; Mismatches
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                             production
                                                                                                                                                                                                                                                                                                                                                                      Hayenga KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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Best Local Similarity
                                                                                                                                        TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001 CURRENT APPLICATION NUMBER: US/09/128,155 CURRENT FILING DATE: 1998-08-03 EARLIER APPLICATION NUMBER: US 60/091,650 EARLIER FILING DATE: 1998-07-02 EARLIER FILING DATE: 1998-07-02 EARLIER FILING DATE: 1997-08-04 EARLIER FILING DATE: 1997-08-04 NUMBER OF SEQ ID NOS: 18
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                                                        FEATURE:
                                                                     ORGANISM: Homo sapiens
                                                                                    TYPE: DNA
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CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 17
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Matches 80
                                                                               Sequence 1, Application US/07638431 Patent No. 5198535 GENERAL INFORMATION:
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APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09128155
Patent No. 6117654
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 GTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAACTTAATAGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 53.3 hes 80; Conservative
                                                                                                                                                                                                                                                                                                           TGTGTCTGACAAATTATTTTGTAAGATACATTTCCTACTTAATGTATCTTGCCTTTTCTA/150442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176373
Charoenvit, Yupin
Hedstrom, Richard
Khusmith, Srisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                 Hoffman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%;
53.3%;
                                                              Stephen L.
                                     Yupin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB of Pred. No. 0.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70;
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APPLICANT:

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; OTHER INFORMATION:
US-07-638-431-1
                                                                                                                           PCT-US92-00018-1
                                                                                                                                             RESULT
                                                                                            Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 295-40 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4673 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                APPLICANT:
                                                                               APPLICANT:
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LIBRARY: Py-la
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                          323
                                                                                                                                                                                                                      356 TAATAGCATATTTCATAGCTATAT 379
                                                                                                                                                                                                                                                   263 TTTTCGAAGAGAAATATTTTTAAATACTTTTTTTAGTGCTTGCATTATTTTTATGATATA 322
                                                                                                                                                                                                                                                                                                               / Match 6.5%;
Local Similarity 64.3%;
les 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE:
TISSUE TYPE: Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                         TATTAACATTCATAAAATATATAT 346
                                                                                                                                                                                                                                                                                  TTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGTTTTTCTTATCAA 355
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    INVENTION:
                                                                                                            Application PC/TUS9200018
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NMRDC Building 1 T-12 National Naval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Py-lambdagt11-2-7 kb genomic expression
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718..3195
                 Rogers IV, William O.
                                                               Charoenvit,
                                                                             Hoffman, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium yoelii
                                   Khusmith,
                                               Hedstrom, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295-4033
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Protective malaria sporozoite surface protein
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                                                             Yupin
                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 4673; Pred. No. 0.93;
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; OTHER INFORMATION:
PCT-US92-00018-1
                                              Sequence 4, Application US/0873
Patent No. 5961971
GENERAL INFORMATION:
APPLICANT: Martin, Frank N.
TITLE OF INVENTION: Biocont
TITLE OF INVENTION: by Pyth
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spevack, Avram D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.2.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
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                  CORRESPONDENCE ADDRESS
                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                  296 TTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCAGTATTGTTTTTTCTTATCAA 355
                                                                                                                                                                                                                                                 356 TAATAGCATATTTCATAGCTATAT 379
                                                                                                                                                                                                                                                                               263 TTTTCGAAGAGAAATATTTTTAAATACTTTTTTAGTGCTTGCATTATTTTTATGATATA 322
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STREET: Medical Center
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LOCATION: 718.
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE TYPE:
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                                                                                                                                  Application US/08731722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17X(NL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: A. David Spevack

NMRDC Building 1 T-12 National Naval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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 Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19920103
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                                  Biocontrol of Fungal Soilborne Pathogens
by Pythium oligandrum
                                                                                                                                                                                                                                                                                                                                                               64.3%;
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                                                                                                                                                                                                                                                                                                                                                               Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                Mismatches
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STREET: 2421 N.W. CITY: Gainesville

2421 N.W. 41st Street, Suite A-1

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US-08-731-722-4 ISOLATE: 17-1
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                                                                                                                                                                                                                                                                                               RESULT
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Best Local Similarity
                                                                                                                                                                                                                                            Sequence 7, Application US/08137175A Patent No. 5777095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 101;
                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                            APPLICANT:
                           STREET: 415
STREET: Washington
CITY: Washington
CTMATE: D.C.
TSA
                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,9
REFERENCE/DOCKET NUMBER:
                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                             692 TACTTTAATAAGAAATAAATAATTAATATT 721
                                                                                                                                                                                                                                                                                                                                                                                                           632 AAGAAATTTTTCAATAGAGAAAGGTTTTATTTTTTAATAGAAAATTGTAATTCTTATTT 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 ATTTCTAAATAATCTGAATTTAAACAGTAGACCCTATGAACCTTTAATAATAGCTAT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCAT 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                             270
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                                                                           419 Seventh Street, N.W.,
                                                                                                                                                                         HANSSON,
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                                                                                                                                                                                            BARBOUR, Alan G. BERGSTROEM, Sven
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SYSTEM: PC-DOS/MS-DOS
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48.1%;
                                                                                                                                              PROPHYLAXIS
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Pred. No. 0.8;
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                                                                           Suite
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                                                                                                    Sequence 7, Application US/08479017 Patent No. 6143872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                    GENERAL INFORMATION:
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1958 base pairs
APPLICANT: HANSSON TITLE OF INVENTION: TITLE OF INVENTION:
                                                 APPLICANT:
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: BA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      185 GTTAGCAGCCTTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          196 ATACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCT 255
                                                                                                                                                                                                                                     376 ATATCAATACTTGACAAA 393
                                                                                                                                                                                                                                                                        125 ATGAAAAAATATTTATTGGGAATAGGTCTAATATTAGCATTAATAGCATGTAAGCAAAAT 184
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralassa "."
                                                                                                                                                                                                                                                                                                                                                                         256 TTAATCATATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGT 315
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LOCATION: 959..18
OTHER INFORMATION:
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LOCATION: 125..949
OTHER INFORMATION:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                          5 ATAATTAGAATTATTATCATTTTATTTTTTTTTAATTTTGCTATTTGTTATTTGTTGATCT 64
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                             BARBOUR, Alan G.
BERGSTROEM, Sven
HANSSON, Lennart
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959..1843
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48.5%;
   IMPROVEMENT IN BORRELIA BURGDORFERI AND PROPHYLAXIS
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Pred. No. 1.
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Best Local Similarity 48.5%;
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REFERENCE/DOCKET NUMBER: BA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/137,175
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
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TELEFAX: 248633
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                          376 ATATCAATACTTGACAAA 393
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LOCATION:
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LOCATION: 959..184
OTHER INFORMATION:
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GTTAGCAGCCTTGATGAA 202
                                                        ATGAAAAATATTTATTGGGAATAGGTCTAATATTAGCATTAATAGCATGTAAGCAAAAT 184
                                                                                    TGGATACATTTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCT 375
                                                                                                                TTAATCATATCCATGGGTGTATTTCTTAACTTAATAGGGGGTTTTCGACGAAGTATATGGT 315
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419 Seventh Street, N.W.,
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959..1843
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Pred. No. 1.5;
0; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          Matches 130;
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APPLICANT: Calabretta, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (215) 568-559
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5775 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                      4598 GTTACCTTGAAAGCTGAATTTATATTTAGTAACTTCTGTGTTAATACTGGATAGCATGAA 4657
                                                                                                                                                                                                                                                                     4538 TTTGTCAAAAAGTAATGATTTCTTGATAATTGTGTAGTGAATGTTTTTTTAGAACCCAGCA 4597
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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4778 TTGAAGTGCCTGTTTGGGATAATGATAGGTAATTTAGATGAATTTAGGGG 4827
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                               244 GTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAACTTAATAGG 293
                                                                                                 184 GCAATTGGTGGGATACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-831
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                   CACATGAGTTCTTGAAGAATAGTCATAACTAGATTAAGATCTGTGTTTTAGTTTAATAGT 477:
                                                                                                                                  19102
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                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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Suite 1800
                                                                                                                                                                                                                                                                                                                                                        Score 34; I
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                          Mismatches
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; STRANDEDNESS:
; TOPOLOGY: 11n;
; MOLECULE TYPE: 1
PCT-US93-06251-29
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                Sequence 1, Application US/09097541 Patent No. 6100092 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 5775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                     4538
                                                                                                                                                                                                                                                                               4658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DIGL9110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    4598
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TELEPHONE: 516-742-4366
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGAAGTGCCTGTTTGGGATAATGATAGGTAATTTAGATGAATTTAGGGG 4827
                                                                                                                                                                      GTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAACTTAATAGG 293
                                                                                                                                                                                                          CACATGAGTTCTTGAAGAATAGTCATAACTAGATTAAGATCTGTGTTTTAGTTTAATAGT
                                                                                                                                                                                                                                         GCAATTGGTGGGATACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGA 243
                                                                                                                                                                                                                                                                                                                                                GTTACCTTGAAAGCTGAATTTATATTTAGTAACTTCTGTGTTAATACTGGATAGCATGAA 4657
                                                                                                                                                                                                                                                                                                                                                                               TTAACAATGATCGCATTAGCTATCTCTATGTCGTCATGGTTTAATATATGGAATAATGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGTCAAAAAGTAATGATTTCTTGATAATTGTGTAGTGAATGTTTTTTAGAACCCAGCA 4597
                                                                                                                                                                                                                                                                             TTAAGCGATCTAGGACATGCTGTTAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130;
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Borysyuk, Mykola
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Pred. No. 3
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                                                                                                                                                                  RESULT
                                                                                Patent No. 5993827
GENERAL INFORMATION:
                                                                                                                        Sequence 13,
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Best Local Similarity 46.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
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NAME: Merkel, William K.
REGISTRATION NUMBER: 40,725
REFERENCE/DOCKET NUMBER: 2915
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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MOLECULE TYPE:
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LENGTH: 446 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                          APPLICANT:
                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                         APPLICANT:
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ATTTTATGCATTGTTTTTTTTTTTAAATAGTTTTTATCGTACTTGTTTTATAAAATATTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 ATACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCT
                                                                                                                                                                                                                             366 TCATTTGT 373
                                                                                                                                                                                                                                                                   436 TGGTATCT 443
                                                                                                                                                                                                                                                                                                           306 AAATATTTATTAAAAAAATATTATTTTTTTGTAAAATATATCATTTACAATGTTTAAAAG
                                                                                                                                                                                                                                                                                                                                               376 ATATCAATACTTGACAAATCATGGATAGCTGTTCTACTAATAATAGGTCATATTGCAATG 435
                                                                                                                                                                                                                                                                                                                                                                                                                             316 TGGATACATTTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 TTAATCATATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGT 315
                                                                                                                                                                                                                                                                                                                                                                                       246 ATATTTATAATAATTTTCTTATTTTTTTTGTATTTATTATGTATTTTTTCGTTTTATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 ATTATTTTATGTGTTATATTATTACTTGATGTATTGGAAATTTTCTCCATTGTTTTTTCT
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 233 SC
CITY: Chicago
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DESCRIPTION: /desc = "APS rDNA sequence"
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                                                                                                                        Application US/08487826B
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Sim, Kim L.
Chitnis, Chetan
Chiller, Louis H.
Miller, David (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borysyuk, Lyudmyla
Raskin, Ilya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Materials and methods for amplifying polynucleotides in plants
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Pred. No. 2;
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Matches
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                    197
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                                  377
                                                                                                                                                                                                                                                                                                 137 GACATGCTGTTAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGA 196
                                                                                                                                                                                                                                                                                                                                                    79 TTAGCTATCTCTA--TGTCGTCATGGTTTAATATGGAATAATGCATTAAGCGATCTAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                    19 TCTTGGATGGATATGATAATATTTATTCTCAGCTTTTCTTTTCCCATTAACAATGATCGCA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 10-SEP CLASSIFICATION: 435
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                                                                                                                                                                                                                                TACTAATTGTTATAGTTGGTTTAAGAAATCTTTATTCGTGGAGTAGAGTTAAAGGATCTT 256
                                                              TAATCATATCCATGGGTGTATTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191;
                           TATCAATACTTGACAAATCATGGATAGCTGTTCTACTAATAATAGGTCATATTGCAAT 434
                                                                                              GGATACATTTCCTAGTCTCAGTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTA 376
                                                                                                                               TTTTAATATAAAATACATATATAAAAATATATATAAAAACACATAC-AAGTACATCCAT 15364
                                                                                                                                                                                                 Newport Beach
: California
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620 Newport Center Drive 16th Floor
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Wellems, Thomas E.
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45.7%;
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Pred. No. 6;
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Patent No. 5608149
GENERAL INFORMATION:

APPLICANT:

Barry, Gerard Kishore, Gane

Sequence 28,

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                    US-08-398-627-28
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                                     RESULT
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/539763
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                       168 TAAATTTTAATATTTTTATAAAAAAATATCGAGCTAAATCATATC
                                                                                                                       397 TGGATAGCTGTTCTACTAATAATAGGTCATATTGCAATGTGGTATC 442
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FILING DATE: 19930712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                           TTTTTTTTTTTTTATCAAAATGATTGGCTGCTATAAAATATCTAATGGTTATTATACA
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Application US/08398627
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Stark, David M.
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Pred. No. 2
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US-08-406-857-2
US-08-406-857-2
; Sequence 2, Application US/08406857
; Patent No. 5608150
; GENERAL INFORMATION:
Timothy W.
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Best Local
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NAME: BONNEY, GLAC.

REGISTRATION NUMBER: 32, YOU
REFERENCE/DOCKET NUMBER: 38-21

REFERENCE/DOCKET NUMBER: 38-21

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION J 537-7286

"FILEPHONE: (314) 537-6047

'714) 7314) 73 NO: 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/
FILING DATE: 12-JUI-1993/
APPLICATION NUMBER: US 07/
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Conner, Timothy W. TITLE OF INVENTION: Fruit Spe
                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 6.0%;
Local Similarity 50.0%;
hes 83; Conservative
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                   STREET:
                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                      GTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATACTTGACAAATCA 396
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               E: Grace L. Bonner, Monsanto Company, BB4F 700 Chesterfield Parkway No. 5608150th
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                                                                                        Fruit Specific Promoters
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Search completed: May 30, 2001, Job time: 3149 sec
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 12-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
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APPLICATION NUMBER: PCT/
FILING DATE: 27-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                           397 TGGATAGCTGTTCTACTAATAATAGGTCATATTGCAATGTGGTATC 442
                                                                                                                                                                108 TTTTTTTTTTTTTATCAAAATGATTGGCTGCTATATAAATATCTAATGGTTATTATACA 167
                                                                                                                                                                                                                                                                            277 TTTCTTAACTTAATAGGGGTTTTCGACGAAGTATATGGTTGGATACATTTCCTAGTCTCA 336
                                                                                          168 TAAATTTTAATATTTTTATAAAAAAATATCGAGCTAAATCATATC 213
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                 Local Similarity
les 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bonner, Grace L. REGISTRATION NUMBER: 32,963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                       GTATTGTTTTTCTTATCAATAATAGCATATTTCATAGCTATATCAATACTTGACAAATCA 396
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Pred. No. 2.6;
O; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                          source
                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library filters for hybridization from the BACPAC Resource Center can be constituted at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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fly), genomic survey sequence.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
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191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
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    from Drosophila melanogaster (fruit
                                                                              melanogaster"
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Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.bbi.ac.uk This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud (Dros BAC) was made by Bac (Dros BAC) was 
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Direct Submission
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                         melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila for manner using these BACs. For further information
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/db_xref="taxon:7227"
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster and please see http://www.fruitfly.org The BDGP Drosophila haron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                            Drosophila melanogaster genome BACN04E04 of DrosBAC library fifty), genomic survey sequence.
Direct Submission
Submitted (23-JUL-1999)
BP 191 91006 EVRY cedex
                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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Determination of this BAC-end Sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
The University of Tokyo, Department of Parasitology 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Tel: 81-3-5449-5378
                                                                                                     Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. FULL. malaria: a database for a full-length enriched from human malaria parasite, Plasmodium falciparum Nucleic Acids Res. 29 (1), 70-71 (2001)
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                                                                                                                                                                                                                                              Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., E,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palme,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVSMEC0004F09f Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEC0004F09f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Suc
,S. Construction and characterization of a full length-enriched
,S. cend-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                 Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                        Clemson University
100 Jordan Hall, C
                                                                                                                                       Clemson University Genomics
                                                                                                                                                                       Development of a genetically and physically for barley genomics Unpublished (2000)
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                                                                                                                                                            Contact: Wing RA
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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/clone="xPFn2716"
/clone="tapen"Sugano Malaria cDNA library"
/clone_tib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
56 c 48 g 148 t 4 other
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/strain="3D7"
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                                                                      CNS0106X 1101 bp DNA GSS 26-JUL-199 Drosophila melanogaster genome survey sequence T7 end of BAC BACN03K20 of DrosbAC library from Drosophila melanogaster (fily), genomic survey sequence.
                                     GSS.
fruit fly.
Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Dipter
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/lab_host="TJC121"
/note="Vector: lambdaZAP; Site
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/clone_lib="Hordeum vulgare seedling
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AL106896
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BACN16D22 of DrosBAC library from Drosophila melanogas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of

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/clone="BACN03K20"
/note="end : T7"
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/plasmid="pBeloBAC11"
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                                                                                                                                                                                                                      AU946120 641 bp DNA GSS 27-JAN-2000
Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-46J23, DNA sequence.
                El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J,
Fraser,C. and Adams,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
Determination of clone end sequences from Trypanosoma brucei GUTat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/note="end : T7"
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/clone_lib="DrosBAC"
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                                                                                                                                                                                                                                                                                                                                                                                ATCGCATTAGCTATCTCTATGTCGTCATGGTTTAATATATGGAATAATGCATTAAGCGAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Unpublished (1999)
Other GSSs: Sheared DNA-46J23.TF
Contact: Najib M. El-Sayed
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/note="Vector: pUCl8; Site_l: Smal; Constructed at The
/note="Vector: pUCl8; Site_l: Smal; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barell, Oxford University
Press, 1999)."
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/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTATTCGTGGAGTAGAGTTAAAGGATCTTTAATCATATCCATGGGTGTATTTCTTAAC 285
                                                                                                                                                                                                                                                                                                                      TTGGTGGTATAAAGAGGAATATTTGC 192
                                                                                                                                                                                                                                                                                                                                                                      GTTCTACTAATAATAGGTCATATTGC 431
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GSS.
fruit fly.
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Drosophila melanogaster genome survey sequence TET3 end
BACR14E13 of RPCI-98 library from Drosophila melanogaste
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                              11y), genomic survey sequence AL066743
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 982)
                                                   AL066743.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope
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AL103027
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/clone="BACN10L03"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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(E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                      TIGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGATACTAATTGTTATAGTTGGTT 217
                                                                                                                                                                                                            TATTGTTTTTCTTAT 352
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                                                                                                                                                                           AWWWTTTTTTWWW 554
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                AL129648
AL129648.1
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14E13"
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147 TAAAAGCAGTGTTGCTCCAATATTCAATCTAGGTCTTGCAATTGGTGGGGATACTAATTGT 206
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Fugu rubripes
Fugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
  Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre. Hinxton, Cambridge, CB10 1SB. UK Email:
                                                                                                                                                                  Fugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Neopterygii; Teleostei; Euteleostei; Teatrandontidae; Fugu.
                                                                                        Tetraodontiformes; Tetraodontoidei; Tetra (bases 1 to 502)
Elgar,G., Clark,M.S., Smith,S., Meek,S., Umrania,Y., Williams,G. and Brenner,S.
                                                                                                                                                                                                                                                                                 AL129567
AL129567.1 GI:6111
GSS; genome survey
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Elgar, G., Clark, M.S., Sn
Umrania, Y., Williams, G.
Centre, Hinxton, Cambridge, biohelp@hgmp.mrc.ac.uk
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                                                                                                                                                                         Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
                                                                        Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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AU086530
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V_type: phagemid
PRIMER: KS
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Eukaryota: Alveolata; Apicomplexa; Haemosporida;
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